ABSTRACT

Various embodiments of the invention include methods and compositions for evaluating the risk of irinotecan toxicity in a patient. In certain embodiments, the methods include detecting a promoter polymorphism in one or both *UGT1A1* genes of the patient. In particular embodiments the promoter polymorphism is a single nucleotide polymorphism and may be in linkage disequilibrium with a *UGT1A1* $(TA)_n$ repeat. The methods may include obtaining a nucleic acid sample from the patient and detecting the presence or absence of a promoter polymorphism. The promoter polymorphism may be at nucleotide position -3440, -3401, -3279, -3177, -3175, or -3156 from the *UGT1A1* gene transcriptional start site. The number of TA repeats can be 5, 6, 7, 8 more TA repeats. In particular embodiments, the promoter polymorphism is a -3440C>A, -3401T>C, -3279G>T, -3177C>G, -3175A>G, -3156G>A polymorphism or any combination thereof. Moreover, in other embodiments, identification of a guanine residue at position –3156 indicates the patient does not have a low level of UGT1A1 activity, and therefore, methods and compositions of the invention concern this identification.